

BIOTECHNOLOGY SYSTEMS BRANCH

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<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/522,727

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☒ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ☐ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ☐ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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RECEIVED 1644
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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/522,727
 DATE: 01/04/2001
 TIME: 08:52:41

Input Set : A:\47577.txt
 Output Set: N:\CRF3\01042001\I522727.raw

Does Not Comply
 Corrected Diskette Needed
 See pp. 1-5

4 <110> APPLICANT: DANA-FARBER CANCER INSTITUTE, INC.
 5 MARASCO, Wayne
 6 MHASHILKAR, Abner
 8 <120> TITLE OF INVENTION: INTRABODY-MEDIATED CONTROL OF IMMUNE
 9 REACTIONS
 11 <130> FILE REFERENCE: 47577 CA
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/522,727
 C--> 14 <141> CURRENT FILING DATE: 2000-03-10
 16 <150> PRIOR APPLICATION NUMBER: 60/059,339
 17 <151> PRIOR FILING DATE: 1997-09-19
 19 <160> NUMBER OF SEQ ID NOS: 55
 21 <170> SOFTWARE: FastSEQ for Windows Version 3.0

ERRORED SEQUENCES

23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 5
 25 <212> TYPE: PRT
 26 <213> ORGANISM: human
 28 <400> SEQUENCE: 1
 29 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 E--> 30 1 5 10 15
 681 <210> SEQ ID NO: 54
 682 <211> LENGTH: 277
 683 <212> TYPE: PRT
 684 <213> ORGANISM: human
 686 <400> SEQUENCE: 54
 687 Met Glu His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
 688 1 5 10 15
 689 Val Leu Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Thr Arg
 690 20 25 30
 691 Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 692 35 40 45
 693 Thr Ser His Trp Met Gln Trp Val Arg Gln Arg Pro Gly Gln Gly Leu
 694 50 55 60
 695 Glu Trp Ile Gly Thr Ile Tyr Pro Gly Asp Gly Asp Thr Arg Tyr Thr
 696 65 70 75 80
 697 Gln Asn Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Thr
 698 85 90 95
 699 Thr Ala Tyr Leu His Leu Ser Ser Leu Ser Ser Glu Asp Ser Ala Val
 E--> 700 100 105 110
 701 Tyr Tyr Cys Ala Arg Asp Glu Ile Thr Thr Val Val Pro Arg Gly Phe
 702 115 120 125
 703 Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
 704 130 135 140
 705 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Leu

Number of amino acids differ:
 - 5 listed
 - 15 shown

Missing amino
 acid numbering

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/522,727

DATE: 01/04/2001
 TIME: 08:52:41

Input Set : A:\47577.txt
 Output Set: N:\CRF3\01042001\I522727.raw

706	145		150		155		160
707	Thr	Gln	Ser	Pro	Ser	Ser	Leu
708							
709	165				170		175
710	Ile	Thr	Cys	His	Ala	Ser	Gln
711							
712	180				185		190
713	Gln	Gln	Lys	Pro	Gly	Asn	Ile
714							
715	195				200		205
716	Asn	Leu	His	Thr	Gly	Val	Pro
717							
718	210				215		220
719	Thr	Gly	Phe	Thr	Leu	Thr	Ile
720							
721	225				230		235
	Thr	Tyr	Tyr	Cys	Gln	Gln	Gly
	245				250		255
	Gly	Thr	Lys	Leu	Glu	Ile	Lys
	260				265		270
	Glu	Lys	Asp	Glu	Leu		

Seg. # 29
 <210> 29
 <211> 32
 <212> PRT
 <213> human

Missing mandatory <220> to <223>
 features to explain "Xaa's" in

<400> 29
 Met Leu Phe Asn Leu Arg (Xaa) (Xaa) Leu Asn Asn Ala Ala Phe Arg His
 1 5 10 15
 Gly His Asn Phe Met Val Arg Asn Phe Arg Cys Gly Gln Pro Leu (Xaa)
 20 25 30

the sequence.

See #10

on the Error

Summary Sheet.

<210> 51
 <211> 837
 <212> DNA
 <213> human

Seg # 51

<220>
 <221> CDS
 <222> (1)...(837)

Missing Mandatory <220> to <223>
 features to explain the "n" at position
 505.

<400> 51

atg gaa cat ctg tgg ttc ttc ctt ctc ctg gtg gca gct ccc aga tgg	48
Met Glu His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp	
1 5 10 15	
gtc ctg tcc cag gtg caa ctg cag cag tca ggg gct gag ctg gca aga	96
Val Leu Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg	
20 25 30	
cct ggg gct tca gtg aag ttg tcc tgc aag gct tct ggc tac acc ttt	144
Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
35 40 45	
act agt cac tgg atg cag tgg gtg aga cag agg cct gga cag ggt ctg	192
Thr Ser His Trp Met Gln Trp Val Arg Gln Arg Pro Gly Gln Gly Leu	
50 55 60	
gaa tgg att ggg act att tat cct gga gat ggt gat act agg tac act	240
Glu Trp Ile Gly Thr Ile Tyr Pro Gly Asp Gly Asp Thr Arg Tyr Thr	
65 70 75 80	
cag aat ttc aag ggc aag gcc aca ttg act gca gat aag tcc tcc acc	288
Gln Asn Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Thr	
85 90 95	
aca gcc tac tta cac ctc agc agc ttg tca tct gaa gac tct gcg gtc	336
Thr Ala Tyr Leu His Leu Ser Ser Leu Ser Ser Glu Asp Ser Ala Val	
100 105 110	
tat tat tgt gca aga gat gag att act acg gtt gta ccc cgg ggg ttt	384
Tyr Tyr Cys Ala Arg Asp Glu Ile Thr Thr Val Val Pro Arg Gly Phe	
115 120 125	
gct tac tgg ggc caa ggg acc tcg gtc acc gtc tcc tca ggt ggc ggt	432
Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly	
130 135 140	
ggc tcg ggc ggt ggt ggc tcg ggt ggc ggc gga tct gag ctc gtg ctc	480
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Leu	
145 150 155 160	
acc caa acc cca acc tcc ctg gct ncc tct ctg gga gac aga gtc acc	528
Thr Gln Thr Pro Thr Ser Leu Ala Xaa Ser Leu Gly Asp Arg Val Thr	
165 170 175	
atc agt tgc agg gca agt cag gac att agc agt tat tta aac tgg tat	576
Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr	
180 185 190	

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p.5

Seq # 52
 <210> 52
 <211> 277
 <212> PRT
 <213> human

Missing mandatory <220> to <223>
 features to explain "Xaa" at

<400> 52
 Met Glu His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
 1 5 10 15
 Val Leu Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg
 20 25 30
 Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 Thr Ser His Trp Met Gln Trp Val Arg Gln Arg Pro Gly Gln Gly Leu
 50 55 60
 Glu Trp Ile Gly Thr Ile Tyr Pro Gly Asp Gly Asp Thr Arg Tyr Thr
 65 70 75 80
 Gln Asn Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Thr
 85 90 95
 Thr Ala Tyr Leu His Leu Ser Ser Leu Ser Ser Glu Asp Ser Ala Val
 100 105 110
 Tyr Tyr Cys Ala Arg Asp Glu Ile Thr Thr Val Val Pro Arg Gly Phe
 115 120 125
 Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly
 130 135 140
 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Leu
 145 150 155 160
 Thr Gln Thr Pro Thr Ser Leu Ala Xaa Ser Leu Gly Asp Arg Val Thr
 165 170 175
 Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr
 180 185 190
 Gln Gln Lys Pro Asp Gly Thr Ile Lys Leu Leu Ile Tyr Tyr Thr Ser
 195 200 205
 Arg Leu Tyr Ser Gly Val Pro Pro Arg Phe Ser Gly Ser Gly Ala Gly
 210 215 220
 Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu Asp Phe Ala
 225 230 235 240
 Thr Tyr Phe Cys Gln Gln Gly Asn Val Ile Pro Tyr Thr Phe Gly Gly
 245 250 255
 Gly Thr Lys Leu Glu Met Lys Arg Ala Asp Ala Ala Pro Thr Val Ser
 260 265 270
 Glu Lys Asp Glu Leu
 275

position 169.

VERIFICATION SUMMARY DATE: 01/04/2001
 PATENT APPLICATION: US/09/522,727 TIME: 08:52:42

Input Set : A:\47577.txt
 Output Set: N:\CRF3\01042001\I522727.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
 L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:30 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5 Found:15 SEQ:1
 L:280 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:29
 L:280 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:29
 L:280 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:29
 L:280 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:29
 L:280 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:29
 L:282 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:29
 L:282 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:29
 L:282 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:29
 L:282 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:29
 M:340 Repeated in SeqNo=29
 L:522 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:51
 L:522 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:51
 L:523 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:51
 M:340 Repeated in SeqNo=51
 L:581 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:52
 L:581 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:52
 L:581 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:52
 L:581 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:52
 L:581 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:52
 L:700 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:54